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## SEQUENCE LISTING

<110> Bogosian, Gregg  
O'Neill, Julia P.  
Smith, Hong Q.

<120> Prevention of Incorporation of Non-Standard Amino Acids into  
Protein

<130> 11916.0059.00PC00

<150> US 60/505,807

<151> 2003-09-25

<160> 16

<170> PatentIn version 3.3

<210> 1

<211> 1344

<212> DNA

<213> Escherichia coli

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caaaatccaa aatatcgcca gatgtcatta ctggagcgtc tggttgaacc ggagcgcgtg 180  
atccagtttc gcgtggtatg ggttgatgat cgcaaccaga tacagggtcaa ccgtgcatgg 240  
cgtgtgcagt tcagctctgc catcgcccg tacaaggcg gtatgcgctt ccatccgtca 300  
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cgtcttatcg aaatcaaagc cagccgcgat ggtcagatgg cagattacgc caaagaattt 900  
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tcgccacccc agaatgaact ggatgttgac gccgcgcac agcttatcgc taatggcggtt 1020
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caggcaggcg tactatttgc accgggtaaa gcggctaata ctggtggcgt cgctacatcg 1140
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gagcaaacca actacgtgca gggcgcgaa attgccgggt ttgtgaagggt tgccgatgcg 1320
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&lt;210&gt; 2

&lt;211&gt; 447

&lt;212&gt; PRT

&lt;213&gt; Escherichia coli

&lt;400&gt; 2

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Arg Asp Pro Asn Gln Thr Glu Phe Ala Gln Ala Val Arg Glu Val Met
          20          25          30
Thr Thr Leu Trp Pro Phe Leu Glu Gln Asn Pro Lys Tyr Arg Gln Met
          35          40          45
Ser Leu Leu Glu Arg Leu Val Glu Pro Glu Arg Val Ile Gln Phe Arg
50          55          60
Val Val Trp Val Asp Asp Arg Asn Gln Ile Gln Val Asn Arg Ala Trp
65          70          75          80
Arg Val Gln Phe Ser Ser Ala Ile Gly Pro Tyr Lys Gly Gly Met Arg
          85          90          95
Phe His Pro Ser Val Asn Leu Ser Ile Leu Lys Phe Leu Gly Phe Glu
          100          105          110
Gln Thr Phe Lys Asn Ala Leu Thr Thr Leu Pro Met Gly Gly Gly Lys
          115          120          125
Gly Gly Ser Asp Phe Asp Pro Lys Gly Lys Ser Glu Gly Glu Val Met
          130          135          140
Arg Phe Cys Gln Ala Leu Met Thr Glu Leu Tyr Arg His Leu Gly Ala
145          150          155          160
Asp Thr Asp Val Pro Ala Gly Asp Ile Gly Val Gly Gly Arg Glu Val
          165          170          175

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Gly Phe Met Ala Gly Met Met Lys Lys Leu Ser Asn Asn Thr Ala Cys  
 180 185 190  
 Val Phe Thr Gly Lys Gly Leu Ser Phe Gly Gly Ser Leu Ile Arg Pro  
 195 200 205  
 Glu Ala Thr Gly Tyr Gly Leu Val Tyr Phe Thr Glu Ala Met Leu Lys  
 210 215 220  
 Arg His Gly Met Gly Phe Glu Gly Met Arg Val Ser Val Ser Gly Ser  
 225 230 235 240  
 Gly Asn Val Ala Gln Tyr Ala Ile Glu Lys Ala Met Glu Phe Gly Ala  
 245 250 255  
 Arg Val Ile Thr Ala Ser Asp Ser Ser Gly Thr Val Val Asp Glu Ser  
 260 265 270  
 Gly Phe Thr Lys Glu Lys Leu Ala Arg Leu Ile Glu Ile Lys Ala Ser  
 275 280 285  
 Arg Asp Gly Arg Val Ala Asp Tyr Ala Lys Glu Phe Gly Leu Val Tyr  
 290 295 300  
 Leu Glu Gly Gln Gln Pro Trp Ser Leu Pro Val Asp Ile Ala Leu Pro  
 305 310 315 320  
 Cys Ala Thr Gln Asn Glu Leu Asp Val Asp Ala Ala His Gln Leu Ile  
 325 330 335  
 Ala Asn Gly Val Lys Ala Val Ala Glu Gly Ala Asn Met Pro Thr Thr  
 340 345 350  
 Ile Glu Ala Thr Glu Leu Phe Gln Gln Ala Gly Val Leu Phe Ala Pro  
 355 360 365  
 Gly Lys Ala Ala Asn Ala Gly Gly Val Ala Thr Ser Gly Leu Glu Met  
 370 375 380  
 Ala Gln Asn Ala Ala Arg Leu Gly Trp Lys Ala Glu Lys Val Asp Ala  
 385 390 395 400  
 Arg Leu His His Ile Met Leu Asp Ile His His Ala Cys Val Glu His  
 405 410 415  
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&lt;210&gt; 3

&lt;211&gt; 1344

&lt;212&gt; DNA

&lt;213&gt; Escherichia coli

- 4 -

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 caaaatccaa aatatcgcca gatgtcatta ctggagcgtc tgggtgaacc ggagcgcgtg 180  
 atccagtttc gcgtgggatg ggttgatgat cgcaaccaga tacaggtcaa ccgtgcatgg 240  
 cgtgtgcagt tcagctctgc catcgccccg tacctgggcg gtatgcgctt ccatccgtca 300  
 gttaaccttt ccattctcaa attcctcggc tttgaacaaa ctttcaaaaa tgccctgact 360  
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 ggtgaagtga tgcgtttttg ccaggcgtg atgactgaac tgtatcgcca cctgggcgcg 480  
 gataccgacg ttccggcagg tgatatcggg gttggtggtc gtgaagtcgg ctttatggcg 540  
 gggatgatga aaaagctctc caacaatacc gcctgcgtct tcaccggtaa gggcctttca 600  
 tttggcggca gtcttattcg cccggaagct accggctacg gtctggttta tttcacagaa 660  
 gcaatgctaa aacgccacgg tatgggtttt gaagggatgc gcgtttccgt ttctggctcc 720  
 ggcaacgtcg ccagtacgc tategaaaaa gcgatggaat ttggtgctcg tgtgatcact 780  
 gcgtcagact ccagcggcac tgtagttgat gaaagcggat tcacgaaaga gaaactggca 840  
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 ggtctggtct atctcgaagg ccaacagccg tgggtctctac cggttgatat cgccctgcct 960  
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 cgtttgcac acatcatgct ggatatccac catgcctgtg ttgagcatgg tgggtgaagg 1260  
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&lt;210&gt; 4

&lt;211&gt; 447

&lt;212&gt; PRT

&lt;213&gt; Escherichia coli

&lt;400&gt; 4

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Met	Asp	Gln	Thr	Tyr	Ser	Leu	Glu	Ser	Phe	Leu	Asn	His	Val	Gln	Lys	1	5	10	15
Arg	Asp	Pro	Asn	Gln	Thr	Glu	Phe	Ala	Gln	Ala	Val	Arg	Glu	Val	Met	20	25	30	
Thr	Thr	Leu	Trp	Pro	Phe	Leu	Glu	Gln	Asn	Pro	Lys	Tyr	Arg	Gln	Met	35	40	45	
Ser	Leu	Leu	Glu	Arg	Leu	Val	Glu	Pro	Glu	Arg	Val	Ile	Gln	Phe	Arg	50	55	60	
Val	Val	Trp	Val	Asp	Asp	Arg	Asn	Gln	Ile	Gln	Val	Asn	Arg	Ala	Trp	65	70	75	80
Arg	Val	Gln	Phe	Ser	Ser	Ala	Ile	Gly	Pro	Tyr	Leu	Gly	Gly	Met	Arg	85	90	95	
Phe	His	Pro	Ser	Val	Asn	Leu	Ser	Ile	Leu	Lys	Phe	Leu	Gly	Phe	Glu	100	105	110	
Gln	Thr	Phe	Lys	Asn	Ala	Leu	Thr	Thr	Leu	Pro	Met	Gly	Gly	Gly	Lys	115	120	125	
Gly	Gly	Ser	Asp	Phe	Asp	Pro	Lys	Gly	Lys	Ser	Glu	Gly	Glu	Val	Met	130	135	140	
Arg	Phe	Cys	Gln	Ala	Leu	Met	Thr	Glu	Leu	Tyr	Arg	His	Leu	Gly	Ala	145	150	155	160
Asp	Thr	Asp	Val	Pro	Ala	Gly	Asp	Ile	Gly	Val	Gly	Gly	Arg	Glu	Val	165	170	175	
Gly	Phe	Met	Ala	Gly	Met	Met	Lys	Lys	Leu	Ser	Asn	Asn	Thr	Ala	Cys	180	185	190	
Val	Phe	Thr	Gly	Lys	Gly	Leu	Ser	Phe	Gly	Gly	Ser	Leu	Ile	Arg	Pro	195	200	205	
Glu	Ala	Thr	Gly	Tyr	Gly	Leu	Val	Tyr	Phe	Thr	Glu	Ala	Met	Leu	Lys	210	215	220	
Arg	His	Gly	Met	Gly	Phe	Glu	Gly	Met	Arg	Val	Ser	Val	Ser	Gly	Ser	225	230	235	240
Gly	Asn	Val	Ala	Gln	Tyr	Ala	Ile	Glu	Lys	Ala	Met	Glu	Phe	Gly	Ala	245	250	255	
Arg	Val	Ile	Thr	Ala	Ser	Asp	Ser	Ser	Gly	Thr	Val	Val	Asp	Glu	Ser	260	265	270	
Gly	Phe	Thr	Lys	Glu	Lys	Leu	Ala	Arg	Leu	Ile	Glu	Ile	Lys	Ala	Ser	275	280	285	
Arg	Asp	Gly	Arg	Val	Ala	Asp	Tyr	Ala	Lys	Glu	Phe	Gly	Leu	Val	Tyr				

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290	295	300
Leu Glu Gly Gln Gln Pro Trp Ser Leu Pro Val Asp Ile Ala Leu Pro		
305	310	315 320
Cys Ala Thr Gln Asn Glu Leu Asp Val Asp Ala Ala His Gln Leu Ile		
	325	330 335
Ala Asn Gly Val Lys Ala Val Ala Glu Gly Ala Asn Met Pro Thr Thr		
	340	345 350
Ile Glu Ala Thr Glu Leu Phe Gln Gln Ala Gly Val Leu Phe Ala Pro		
	355	360 365
Gly Lys Ala Ala Asn Ala Gly Gly Val Ala Thr Ser Gly Leu Glu Met		
	370	375 380
Ala Gln Asn Ala Ala Arg Leu Gly Trp Lys Ala Glu Lys Val Asp Ala		
385	390	395 400
Arg Leu His His Ile Met Leu Asp Ile His His Ala Cys Val Glu His		
	405	410 415
Gly Gly Glu Gly Glu Gln Thr Asn Tyr Val Gln Gly Ala Asn Ile Ala		
	420	425 430
Gly Phe Val Lys Val Ala Asp Ala Met Leu Ala Gln Gly Val Ile		
	435	440 445

&lt;210&gt; 5

&lt;211&gt; 1101

&lt;212&gt; DNA

&lt;213&gt; Bacillus cereus

&lt;400&gt; 5

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gctcttggtg gaacaagaat gtggacatat gattctgaag aagcggcgat tgaagatgca	180
ttgcgtcttg caaaagggat gacatacaaa aacgcagcag ctggttttaa cttaggtggt	240
gcgaaaacag taattatcgg tgatcctcgt aaagataaga gcgaagcaat gttccgtgca	300
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tcattcgggt cttctggtaa cccatctccg gtaactgcat acggtgttta ccgtgggatg	480
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caaggcggtg gtaacgtagc atatcaccta tgcaaacatt tacacgctga aggagcaaaa	600

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ttaatcggtta cagatattaa taaagaagct gtacaacgtg ctgtagaaga attcggtgca    660
tcagcagttg aaccaaataa aatttacggt gttgaatgcg atatttacgc accatgtgca    720
ctaggcgcaa cagttaatga tgaaactatt ccacaactta aagcaaaagt aatcgcaggt    780
tctgcaaata accaattaa agaagatcgt catggtgaca tcattcatga aatgggtatt    840
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tatggatata atagagaacg tgcactaaaa cgtgttgagt ctatttatga cagcattgca    960
aaagtaatcg aaatttcaaa acgcgatggc atagcaactt atgtagcggc agatcgtcta   1020
gctgaagagc gcattgcaag cttgaagaat tctcgtagca cttacttacg caacgggtcac   1080
gatattatta gccgtcgcta a                                           1101

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&lt;210&gt; 6

&lt;211&gt; 366

&lt;212&gt; PRT

&lt;213&gt; Bacillus cereus

&lt;400&gt; 6

```

Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln
1           5           10           15

```

```

Val Val Phe Cys Gln Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala
          20           25           30

```

```

Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp
          35           40           45

```

```

Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala
          50           55           60

```

```

Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly
65           70           75           80

```

```

Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala
          85           90           95

```

```

Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr
          100          105          110

```

```

Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile
          115          120          125

```

```

His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser
          130          135          140

```

```

Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met
145          150          155          160

```

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Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys  
 165 170 175  
 Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys  
 180 185 190  
 His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys  
 195 200 205  
 Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu  
 210 215 220  
 Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala  
 225 230 235 240  
 Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys  
 245 250 255  
 Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly  
 260 265 270  
 Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile  
 275 280 285  
 Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn  
 290 295 300  
 Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala  
 305 310 315 320  
 Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala  
 325 330 335  
 Ala Asp Arg Leu Ala Glu Glu Arg Ile Ala Ser Leu Lys Asn Ser Arg  
 340 345 350  
 Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg  
 355 360 365

&lt;210&gt; 7

&lt;211&gt; 1098

&lt;212&gt; DNA

&lt;213&gt; Bacillus subtilis

&lt;400&gt; 7

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 ggcggaacga gaatgtggac atatgaaaat gaagaagcgg caattgaaga cgcgctcaga 180  
 ctggcaagag gcatgacctt taaagacgcg gctgcaggcc taaaccttgg cggcggaataa 240  
 acagtaataa tcggcgatcc acgcaaagac aaaaatgaag aaatgttccg cgcgtttggc 300



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cgctatattc aaggactgaa cggcagatac attacagctg aagatgtggg tacaacgggt 360
gaggatatgg acattattca tgatgaaaca gactatgtca cagggatttc tcctgctttc 420
ggctcttctg gaaatccatc tccagttaca gcgtacgggg tgtacagagg aatgaaagca 480
gccgctaaag ctgctttcgg aaccgactct cttgaagggg aaaccatcgc tgtacagggt 540
gtaggggaatg tggcctacaa cctatgccgc cacctgcatg aagaaggggc aaacttaatc 600
gttacggata tcaacaaaca gtcagtacag cgcgcagttg aagatttttg cggcctgtcg 660
gttgatccgg aagagattta ttcacaagag tgcgatattt atgctccgtg cgcccttgga 720
gcgacaatca acgacgacac cattaaacag ctgaaggcga aagtcacgc ggggtgcggct 780
aataaccaat taaaagaaac gcgccatggc gatcaaattc acgaaatggg tatcgtttac 840
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tataatgcag aacgtgcatt gaaaaaagt gaaggcattt acggcaatat tgagcgtgta 960
cttgagattt ctcagcgtga cggcattcca acatatttag cagctgaccg cttggcagag 1020
gaacggattg aacgcatgcg ccgctcaaga agccagtttt tgcaaaacgg ccacagtgtg 1080
ttaagcagac gttaatag 1098

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&lt;210&gt; 8

&lt;211&gt; 364

&lt;212&gt; PRT

<213> *Bacillus subtilis*

&lt;400&gt; 8

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Met Glu Leu Phe Lys Tyr Met Glu Lys Tyr Asp Tyr Glu Gln Leu Val
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Phe Cys Gln Asp Glu Gln Ser Gly Leu Lys Ala Ile Ile Ala Ile His
20           25           30

Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp Thr Tyr
35           40           45

Glu Asn Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala Arg Gly
50           55           60

Met Thr Tyr Lys Asp Ala Ala Ala Gly Leu Asn Leu Gly Gly Gly Lys
65           70           75           80

Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Asn Glu Glu Met Phe
85           90           95

Arg Ala Phe Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr Ile Thr
100          105          110

```

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Ala Glu Asp Val Gly Thr Thr Val Glu Asp Met Asp Ile Ile His Asp  
 115 120 125  
 Glu Thr Asp Tyr Val Thr Gly Ile Ser Pro Ala Phe Gly Ser Ser Gly  
 130 135 140  
 Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met Lys Ala  
 145 150 155 160  
 Ala Ala Lys Ala Ala Phe Gly Thr Asp Ser Leu Glu Gly Lys Thr Ile  
 165 170 175  
 Ala Val Gln Gly Val Gly Asn Val Ala Tyr Asn Leu Cys Arg His Leu  
 180 185 190  
 His Glu Glu Gly Ala Asn Leu Ile Val Thr Asp Ile Asn Lys Gln Ser  
 195 200 205  
 Val Gln Arg Ala Val Glu Asp Phe Gly Ala Arg Ala Val Asp Pro Glu  
 210 215 220  
 Glu Ile Tyr Ser Gln Glu Cys Asp Ile Tyr Ala Pro Cys Ala Leu Gly  
 225 230 235 240  
 Ala Thr Ile Asn Asp Asp Thr Ile Lys Gln Leu Lys Ala Lys Val Ile  
 245 250 255  
 Ala Gly Ala Ala Asn Asn Gln Leu Lys Glu Thr Arg His Gly Asp Gln  
 260 265 270  
 Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile Asn Ala  
 275 280 285  
 Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn Ala Glu  
 290 295 300  
 Arg Ala Leu Lys Lys Val Glu Gly Ile Tyr Gly Asn Ile Glu Arg Val  
 305 310 315 320  
 Leu Glu Ile Ser Gln Arg Asp Gly Ile Pro Thr Tyr Leu Ala Ala Asp  
 325 330 335  
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 Phe Leu Gln Asn Gly His Ser Val Leu Ser Arg Arg  
 355 360

<210> 9  
 <211> 1062  
 <212> DNA  
 <213> Nostoc sp.

<400> 9

- 11 -

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ggagccacaa ggctttatcc ttatatcaat gaagaagccg ccttaagaga tgctttgcgt      180
ttgagtcggg ggatgactta taaagcagct tgcgctaaca ttcccgcagg cggaggcaaa      240
gccgttatta ttgccaatcc cgaagataaa acagatgaaa tgttgagagc ttatggacgc      300
tttgtggaaa gtctcaaagg tagatttatt accgggcaag atgtgaatat cactccacaa      360
gatgtccgca caattaaaca agaaaccaat tatgtagttg gtgtggaaga aaaatctggt      420
gggcctgctc ctatcacagc tttaggcgta tttttaggta ttaaagctgc tgtagaattt      480
cgctggcaaa ctaaaaatat tgaagggatg acagttgccg ttcaagggtt aggaaatggt      540
ggtcagaatc tctgccgaca cttacatgaa aatgggataa agcttatagt tgctgatttt      600
agttctgaaa aaacagcaga aataaaacac ctttttggtg ctacagtagt agagccagat      660
gaaatttact cacaaaatgt agacatat ttccctgtg ctatgggagg aattattaac      720
agtcaacaaa ttcccact acaagccaaa attattgctg gtgctgccaa taaccagtta      780
gataatgagc gtctgcatgg tcaaagatta gtagaaaaag atatcctcta ctgtcctgat      840
tatgtaatca atgctgggtg tatcatcaac gtttataacg aaatgattgg ctatgaagaa      900
gataaggcct tcaagcaagt taataatatt tacgacacat tattagcaat tttcaatatt      960
gctcaacaac aaagcattac tactaatgat gcttcaaac ggcttgacaga tgaaaggatt     1020
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<210> 10  
 <211> 353  
 <212> PRT  
 <213> Nostoc sp.

<400> 10

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Met Gln Leu Phe Glu Thr Val Arg Glu Met Gly His Glu Gln Val Leu
1              5              10              15

```

```

Tyr Cys His Gly Lys Asn Pro Asp Ile Arg Ala Ile Ile Ala Ile His
          20              25              30

```

```

Asp Thr Thr Leu Gly Pro Ala Met Gly Ala Thr Arg Leu Tyr Pro Tyr
          35              40              45

```

```

Ile Asn Glu Glu Ala Ala Leu Arg Asp Ala Leu Arg Leu Ser Arg Gly
          50              55              60

```

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Met	Thr	Tyr	Lys	Ala	Ala	Cys	Ala	Asn	Ile	Pro	Ala	Gly	Gly	Gly	Lys	65	70	75	80
Ala	Val	Ile	Ile	Ala	Asn	Pro	Glu	Asp	Lys	Thr	Asp	Glu	Met	Leu	Arg	85	90	95	
Ala	Tyr	Gly	Arg	Phe	Val	Glu	Ser	Leu	Lys	Gly	Arg	Phe	Ile	Thr	Gly	100	105	110	
Gln	Asp	Val	Asn	Ile	Thr	Pro	Gln	Asp	Val	Arg	Thr	Ile	Lys	Gln	Glu	115	120	125	
Thr	Asn	Tyr	Val	Val	Gly	Val	Glu	Glu	Lys	Ser	Gly	Gly	Pro	Ala	Pro	130	135	140	
Ile	Thr	Ala	Leu	Gly	Val	Phe	Leu	Gly	Ile	Lys	Ala	Ala	Val	Glu	Phe	145	150	155	160
Arg	Trp	Gln	Thr	Lys	Asn	Ile	Glu	Gly	Met	Thr	Val	Ala	Val	Gln	Gly	165	170	175	
Leu	Gly	Asn	Val	Gly	Gln	Asn	Leu	Cys	Arg	His	Leu	His	Glu	Asn	Gly	180	185	190	
Ile	Lys	Leu	Ile	Val	Ala	Asp	Phe	Ser	Ser	Glu	Lys	Thr	Ala	Glu	Ile	195	200	205	
Lys	His	Leu	Phe	Gly	Ala	Thr	Val	Val	Glu	Pro	Asp	Glu	Ile	Tyr	Ser	210	215	220	
Gln	Asn	Val	Asp	Ile	Phe	Ser	Pro	Cys	Ala	Met	Gly	Gly	Ile	Ile	Asn	225	230	235	240
Ser	Gln	Thr	Ile	Pro	Gln	Leu	Gln	Ala	Lys	Ile	Ile	Ala	Gly	Ala	Ala	245	250	255	
Asn	Asn	Gln	Leu	Asp	Asn	Glu	Arg	Leu	His	Gly	Gln	Arg	Leu	Val	Glu	260	265	270	
Lys	Asp	Ile	Leu	Tyr	Cys	Pro	Asp	Tyr	Val	Ile	Asn	Ala	Gly	Gly	Ile	275	280	285	
Ile	Asn	Val	Tyr	Asn	Glu	Met	Ile	Gly	Tyr	Glu	Glu	Asp	Lys	Ala	Phe	290	295	300	
Lys	Gln	Val	Asn	Asn	Ile	Tyr	Asp	Thr	Leu	Leu	Ala	Ile	Phe	Asn	Ile	305	310	315	320
Ala	Gln	Gln	Gln	Ser	Ile	Thr	Thr	Asn	Asp	Ala	Ser	Lys	Arg	Leu	Ala	325	330	335	
Asp	Glu	Arg	Ile	Met	Lys	Ala	Arg	Ile	Asn	Lys	Asn	Gln	Leu	Ile	Ala	340	345	350	
Ala																			

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<210> 11  
 <211> 1044  
 <212> DNA  
 <213> *Shewanella oneidensis*

<400> 11  
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 aaagaaagtg gcttaaaagc cattattgcc atccataata ccaatttagg ccctgctgtg 120  
 ggtggatgcc ggatgtggaa ctaccaatcc gatgacgaag ccctgacaga cgtattacgc 180  
 ctctcccgtg gtatgactta caaaaacgcg ctcgctgggt taaccatggg cggtggtaaa 240  
 tcagtgatta ttgccgatcc taagcgccct gaccgcgaag ccctcttccg tgcttttggc 300  
 cgttttatca atagtctcg tggacgttac tattccgcag aagacgttgg caccacgaca 360  
 gctgatatta tgatcgccca tcaagaaacg ccctatatgg cggggcctga aggcaagagt 420  
 ggcgatcctt ctccgtttac ggcactaggt acttatttag gtatcaaggc cgcggttaaa 480  
 cataagctcg atttagacag cttaaagggc cttaagatcg ccgttcaagg tggtggccat 540  
 gtgggttatt atctgtgtaa acatctacat gaagaagggt cacagctaatt tgttaccgat 600  
 attcatcagg cgtcacttga taaagtgggt accgactttg gtgctaccgt tggtgcacca 660  
 caggatatct acgccaaga cgtcgatgtg tacgccccat gcgcactagg tgcgacctta 720  
 aacgatgtta ccctgccact actcaaagct aagattgttg caggttgtgc caacaaccaa 780  
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 aaatcagaag ctaaggtcag agaaatctac aacacgctgc tgaagatttt tgctaaagcc 960  
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<210> 12  
 <211> 347  
 <212> PRT  
 <213> *Shewanella oneidensis*

<400> 12

Met Ala Val Phe Asn His Val Ser Phe Asp Glu His Glu Gln Val Val  
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Phe Cys His Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala Ile His

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20					25					30					
Asn	Thr	Asn	Leu	Gly	Pro	Ala	Val	Gly	Gly	Cys	Arg	Met	Trp	Asn	Tyr
		35					40					45			
Gln	Ser	Asp	Asp	Glu	Ala	Leu	Thr	Asp	Val	Leu	Arg	Leu	Ser	Arg	Gly
	50					55					60				
Met	Thr	Tyr	Lys	Asn	Ala	Leu	Ala	Gly	Leu	Thr	Met	Gly	Gly	Gly	Lys
65						70					75				80
Ser	Val	Ile	Ile	Ala	Asp	Pro	Lys	Arg	Pro	Asp	Arg	Glu	Ala	Leu	Phe
				85					90					95	
Arg	Ala	Phe	Gly	Arg	Phe	Ile	Asn	Ser	Leu	Gly	Gly	Arg	Tyr	Tyr	Ser
			100					105					110		
Ala	Glu	Asp	Val	Gly	Thr	Thr	Thr	Ala	Asp	Ile	Met	Ile	Ala	His	Gln
		115					120					125			
Glu	Thr	Pro	Tyr	Met	Ala	Gly	Leu	Glu	Gly	Lys	Ser	Gly	Asp	Pro	Ser
	130					135					140				
Pro	Phe	Thr	Ala	Leu	Gly	Thr	Tyr	Leu	Gly	Ile	Lys	Ala	Ala	Val	Lys
145						150					155				160
His	Lys	Leu	Asp	Leu	Asp	Ser	Leu	Lys	Gly	Leu	Lys	Ile	Ala	Val	Gln
				165					170					175	
Gly	Val	Gly	His	Val	Gly	Tyr	Tyr	Leu	Cys	Lys	His	Leu	His	Glu	Glu
			180					185					190		
Gly	Ala	Gln	Leu	Ile	Val	Thr	Asp	Ile	His	Gln	Ala	Ser	Leu	Asp	Lys
		195					200					205			
Val	Ala	Thr	Asp	Phe	Gly	Ala	Thr	Val	Val	Ala	Pro	Gln	Asp	Ile	Tyr
	210					215					220				
Ala	Gln	Asp	Val	Asp	Val	Tyr	Ala	Pro	Cys	Ala	Leu	Gly	Ala	Thr	Leu
225						230					235				240
Asn	Asp	Val	Thr	Leu	Pro	Leu	Leu	Lys	Ala	Lys	Ile	Val	Ala	Gly	Cys
				245					250					255	
Ala	Asn	Asn	Gln	Leu	Ala	Glu	Val	Arg	His	Gly	Glu	Gln	Leu	Lys	Glu
			260					265					270		
Met	Gly	Ile	Leu	Tyr	Ala	Pro	Asp	Tyr	Val	Ile	Asn	Ala	Gly	Gly	Ile
		275					280					285			
Ile	Asn	Val	Ser	Phe	Glu	Lys	Asp	Tyr	Asp	Ala	Ala	Lys	Ser	Glu	Ala
	290						295				300				
Lys	Val	Arg	Glu	Ile	Tyr	Asn	Thr	Leu	Leu	Lys	Ile	Phe	Ala	Lys	Ala
305						310					315				320



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&lt;400&gt; 14

Met	Thr	Asp	Val	Ser	Asp	Gly	Val	Leu	His	Thr	Leu	Phe	Arg	Ser	Asp	1	5	10	15
Gln	Gly	Gly	His	Glu	Gln	Val	Val	Leu	Cys	Gln	Asp	Arg	Ala	Thr	Gly	20	25	30	
Leu	Lys	Ala	Val	Ile	Ala	Ile	His	Ser	Thr	Ala	Leu	Gly	Pro	Ala	Leu	35	40	45	
Gly	Gly	Thr	Arg	Phe	Tyr	Pro	Tyr	Ala	Ser	Glu	Glu	Glu	Ala	Val	Ala	50	55	60	
Asp	Ala	Leu	Asn	Leu	Ala	Arg	Gly	Met	Ser	Tyr	Lys	Asn	Ala	Met	Ala	65	70	75	80
Gly	Leu	Asp	His	Gly	Gly	Gly	Lys	Ala	Val	Ile	Ile	Gly	Asp	Pro	Glu	85	90	95	
Arg	Ile	Lys	Thr	Glu	Glu	Leu	Leu	Leu	Ala	Tyr	Gly	Arg	Phe	Val	Ala	100	105	110	
Ser	Leu	Gly	Gly	Arg	Tyr	Val	Thr	Ala	Cys	Asp	Val	Gly	Thr	Tyr	Val	115	120	125	
Ala	Asp	Met	Asp	Val	Val	Ala	Arg	Glu	Cys	Arg	Trp	Thr	Thr	Gly	Arg	130	135	140	
Ser	Pro	Glu	Asn	Gly	Gly	Ala	Gly	Asp	Ser	Ser	Val	Leu	Thr	Ala	Phe	145	150	155	160
Gly	Val	Phe	Gln	Gly	Met	Arg	Ala	Ser	Ala	Gln	His	Leu	Trp	Gly	Asp	165	170	175	
Pro	Thr	Leu	Arg	Gly	Arg	Lys	Val	Gly	Ile	Ala	Gly	Val	Gly	Lys	Val	180	185	190	
Gly	Arg	His	Leu	Val	Arg	His	Leu	Leu	Asp	Asp	Gly	Ala	Glu	Val	Val	195	200	205	
Ile	Thr	Asp	Val	Arg	Thr	Asp	Ser	Val	Gln	Arg	Ile	Leu	Asp	Gln	His	210	215	220	
Pro	Thr	Gly	Val	Thr	Ala	Val	Ala	Asp	Thr	Asp	Ala	Leu	Ile	Arg	Val	225	230	235	240
Asp	Gly	Leu	Asp	Ile	Tyr	Ala	Pro	Cys	Ala	Leu	Gly	Gly	Ala	Leu	Asn	245	250	255	
Asp	Asp	Ser	Val	Thr	Val	Leu	Thr	Ala	Lys	Ile	Val	Cys	Gly	Ala	Ala	260	265	270	
Asn	Asn	Gln	Leu	Ala	His	Thr	Gly	Val	Glu	Lys	Asp	Leu	Ala	Asp	Arg				



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275	280	285
Gly Ile Leu Tyr Ala Pro Asp Tyr Val Val Asn Ala Gly Gly Val Ile		
290	295	300
Gln Val Ala Asp Glu Leu His Gly Phe Asp Phe Asp Arg Cys Lys Ala		
305	310	315
Lys Ala Ala Lys Ile Phe Asp Thr Thr Leu Ala Ile Phe Ala Arg Ala		
325	330	335
Lys Glu Asp Gly Ile Pro Pro Ala Ala Ala Asp Arg Ile Ala Glu		
340	345	350
Gln Arg Met Ala Glu Ala Arg Arg Gly		
355	360	

&lt;210&gt; 15

&lt;211&gt; 1347

&lt;212&gt; DNA

&lt;213&gt; Nitrosomonas europaea

&lt;400&gt; 15

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cccgaattcc tgcaggccgt ttcagaagtc attgaaagct tgtggccttt tatcgtcgat	120
cattctcggt acgctgagca ggggttgctg gatcggctga tcgagccgga gcgcatgatc	180
atattccggg tggcgtgggt ggatgatcgg ggtgaagtca aggtcaatcg ggggtaccgc	240
attcaatata attcggcgat cggcccatatc aaggggggta cgcgcttcca tccgtcagtc	300
aacctttcca ttctcaaatt ccttgcatct gagcagactt tcaagaatgc actgacaaca	360
ttgccgatgg gaggaggcaa ggggtggatcg gatcttgatc ccaagggtaa aagtcccggg	420
gaaatcatgc gcttctgcc aagcgtatgc gccgaactgt tccggcatgt cgggtgcggat	480
acggatgtac ctgccggaga catcgggtgt ggcggacggg aagtcggcta catggctggt	540
atgggtcaaga agctgaccaa ccgttcggac tgtgtattta ccggcaaagg attgaccttc	600
gggggatcgc tgctgcggcc ggaagctacc gggtagggtc tgggtctattt tgccgaagag	660
atgctgaatc actccgggtt ttcatgaaa ggcattgcggg tatccgtatc cgggtccggg	720
aacgtggcac agtttgccat tgacaaggcc atgtcgtcgt gtgccaaagt agtcacgggt	780
tcagattcga gtggtacggg ggtggatgaa gccggtttta caccagaaaa actggcaatt	840
ctggccgaag tcaagaatcg tctctacggg cgtgtcaatg aatttgctga acgggtggaa	900
gcacagttcc ttccgggtga aaaaccgtgg catgtgccgg tggatgtcgc ttgcccctgt	960

- 18 -

gcgacccaga atgaactgaa cgaaaacgac gccgcaatac tgatcaggaa tgggtgcaat 1020  
 tgtgtggccg aggggtgcaa tatgccatgc actgcaggtg ccgtggaacg attccatcat 1080  
 gcgaaagtac tgtttgcacc tggcaaggcg agcaacgcag gcggagtggc tacctcgggt 1140  
 ctggaaatga gccagcaggc catgcgactt tcctggacga gcggagaagt cgatatgcgg 1200  
 ttacaggaaa tcatgcgtgc cattcatcat tcctgcaccg aatacggcaa gaagcctgac 1260  
 ggtacggtca actatgtgga tgggtgccaat gttgccggat ttgtgaaagt ggccgaggca 1320  
 atgctggcgc aaggggtgat ctgataa 1347

&lt;210&gt; 16

&lt;211&gt; 447

&lt;212&gt; PRT

&lt;213&gt; Nitrosomonas europaea

&lt;400&gt; 16

Met Lys Tyr Asn Ser Ile Glu Glu Phe Lys Asn Tyr Val Ser Glu Arg  
 1 5 10 15  
 Asn Pro Gly Gln Pro Glu Phe Leu Gln Ala Val Ser Glu Val Ile Glu  
 20 25 30  
 Ser Leu Trp Pro Phe Ile Val Asp His Ser Arg Tyr Ala Glu Gln Gly  
 35 40 45  
 Leu Leu Asp Arg Leu Ile Glu Pro Glu Arg Met Ile Ile Phe Arg Val  
 50 55 60  
 Ala Trp Val Asp Asp Arg Gly Glu Val Lys Val Asn Arg Gly Tyr Arg  
 65 70 75 80  
 Ile Gln Tyr Asn Ser Ala Ile Gly Pro Tyr Lys Gly Gly Thr Arg Phe  
 85 90 95  
 His Pro Ser Val Asn Leu Ser Ile Leu Lys Phe Leu Ala Phe Glu Gln  
 100 105 110  
 Thr Phe Lys Asn Ala Leu Thr Thr Leu Pro Met Gly Gly Gly Lys Gly  
 115 120 125  
 Gly Ser Asp Phe Asp Pro Lys Gly Lys Ser Pro Gly Glu Ile Met Arg  
 130 135 140  
 Phe Cys Gln Ala Tyr Ala Ala Glu Leu Phe Arg His Val Gly Ala Asp  
 145 150 155 160  
 Thr Asp Val Pro Ala Gly Asp Ile Gly Val Gly Gly Arg Glu Val Gly  
 165 170 175  
 Tyr Met Ala Gly Met Val Lys Lys Leu Thr Asn Arg Ser Asp Cys Val

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180						185						190					
Phe	Thr	Gly	Lys	Gly	Leu	Thr	Phe	Gly	Gly	Ser	Leu	Leu	Arg	Pro	Glu		
		195					200					205					
Ala	Thr	Gly	Tyr	Gly	Leu	Val	Tyr	Phe	Ala	Glu	Glu	Met	Leu	Asn	His		
	210					215					220						
Ser	Gly	Cys	Ser	Leu	Lys	Gly	Met	Arg	Val	Ser	Val	Ser	Gly	Ser	Gly		
225					230					235					240		
Asn	Val	Ala	Gln	Phe	Ala	Ile	Asp	Lys	Ala	Met	Ser	Leu	Gly	Ala	Lys		
				245					250					255			
Val	Val	Thr	Val	Ser	Asp	Ser	Ser	Gly	Thr	Val	Val	Asp	Glu	Ala	Gly		
			260					265					270				
Phe	Thr	Pro	Glu	Lys	Leu	Ala	Ile	Leu	Ala	Glu	Val	Lys	Asn	Arg	Leu		
		275					280					285					
Tyr	Gly	Arg	Val	Asn	Glu	Phe	Ala	Glu	Arg	Val	Glu	Ala	Gln	Phe	Leu		
	290					295					300						
Pro	Gly	Glu	Lys	Pro	Trp	His	Val	Pro	Val	Asp	Val	Ala	Leu	Pro	Cys		
305					310					315					320		
Ala	Thr	Gln	Asn	Glu	Leu	Asn	Glu	Asn	Asp	Ala	Ala	Ile	Leu	Ile	Arg		
				325					330					335			
Asn	Gly	Ala	Asn	Cys	Val	Ala	Glu	Gly	Ala	Asn	Met	Pro	Cys	Thr	Ala		
			340					345				350					
Gly	Ala	Val	Glu	Arg	Phe	His	His	Ala	Lys	Val	Leu	Phe	Ala	Pro	Gly		
		355					360					365					
Lys	Ala	Ser	Asn	Ala	Gly	Gly	Val	Ala	Thr	Ser	Gly	Leu	Glu	Met	Ser		
	370					375					380						
Gln	Gln	Ala	Met	Arg	Leu	Ser	Trp	Thr	Ser	Gly	Glu	Val	Asp	Met	Arg		
385					390					395					400		
Leu	Gln	Glu	Ile	Met	Arg	Ala	Ile	His	His	Ser	Cys	Thr	Glu	Tyr	Gly		
				405					410					415			
Lys	Lys	Pro	Asp	Gly	Thr	Val	Asn	Tyr	Val	Asp	Gly	Ala	Asn	Val	Ala		
			420					425					430				
Gly	Phe	Val	Lys	Val	Ala	Glu	Ala	Met	Leu	Ala	Gln	Gly	Val	Ile			
		435					440					445					